

EXHIBIT 2

HG52.apr

Section 1					
	1	10	20	30	45
AAH18130_PAR1L	(1)	-----MRSPSAAWLLGAAILLASA	LSCSGTIQGTNRRSKGRSLIG		
NP_001983_PAR1	(1)	MGPRLLLLVAACFSLCGPLLSA	RTRARRPESKATNATLDPRSFL		
NP_835230_P2Y8	(1)	-	-		
TransBD243560_HG52	(1)	-	-		
NP_004092_PAR3	(1)	-	MKALIFAAAGLLLLPTFCQSGM	ENDTNNLAKPTLPIK	
NP_005287_P2Y9	(1)	-	-		
P79928_XP2Y	(1)	-	-		
Consensus	(1)	-	-		
Section 2					
	46	60	70	80	90
AAH18130_PAR1L	(41)	-	-	KVDGTSHTVGKVTVETVFSVDE	
NP_001983_PAR1	(46)	RNPNDKYEPFWEDEEKNESGL	TEYRLVSINKSSPLQQLPAFISE		
NP_835230_P2Y8	(1)	-	-	MQVPNSTGPDN	
TransBD243560_HG52	(1)	-	-	MQVPNSTGPDN	
NP_004092_PAR3	(39)	TFRGAPPNSFEFPFSALEGWTG	AATVKIKCP-EESASHLHVKN		
NP_005287_P2Y9	(1)	-	-	MGDRRFIDFQFQDSNSSLRPR	LGNA
P79928_XP2Y	(1)	-	-	MTEDIMATSYPFTLTTPYLP	MKELMNLTN
Consensus	(46)	-	-	M V	D
Section 3					
	91	100	110	120	135
AAH18130_PAR1L	(64)	F SASVLTGKLTTVFLPIVYT	TIVEVVGLESNGMALWWFL	FRTKKKH	
NP_001983_PAR1	(91)	DASGYLTSSWLTLFVPSVY	TGVEVVSLELNIMAVV	ILKMKVKK	
NP_835230_P2Y8	(12)	ATLQMERNP	IAVALPVVYSLEVAAVSIEGNLF	SLWVL	CRRMGP
TransBD243560_HG52	(12)	ATLQMERNP	IAVALPVVYSLEVAAVSIEGNLF	SLWVL	CRRMGP
NP_004092_PAR3	(83)	ATMGYETSSLSTKLIPAIYLL	VFGVANAVT	MLFFRT	SI
NP_005287_P2Y9	(28)	NNTCIVDDSF	KYNLNGAVYSV	ILGLITNSVS	LFVCFRMK
P79928_XP2Y	(32)	EDTCVFDEGFKF	LLPVSYS	AVEMVG	ELNTAAMWIEIAKMR
Consensus	(91)	TL ML	V LPVVYSLV	VFGV	WPF
Section 4					
	136	150	160	170	180
AAH18130_PAR1L	(109)	PAVITYMANLALADL	LSVIWFPLKTA	YHIHGNNWLYGEALCN	VALIG
NP_001983_PAR1	(136)	PAVYYMLHLATA	DVLEVS	PLPKTISYYFSGSD	WQEGSELCR
NP_835230_P2Y8	(57)	PSVLEM	INLSVTDLMLAS	VLPHQI	YYHCNRHHWVG
TransBD243560_HG52	(57)	PSVLEM	INLSVTDLMLAS	VLPHQI	YYHCNRHHWVG
NP_004092_PAR3	(127)	CITV	YEYTNLA	IADFECV	TLPEFKIAYH
NP_005287_P2Y9	(73)	ETAI	LEITNLAVS	DLLFV	CVTLPEFKI
P79928_XP2Y	(77)	PTVYMFNL	ALSDTLYV	LSLPTLV	YYADKNNWPF
Consensus	(136)	PTVIFM	NLA	VADLLFV	WPFGEV

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Section 5

(181)	181	190	200	210	225
AAH18130_PAR1L (154)	FFYGNMYCSILFMTCLSMQRYWVIVNIPMGHSRKK	-ANIAIGISLA			
NP_001983_PAR1 (181)	AFYCNMYASILLMTVISIDRF	LAVVYPMOSLSWRTLGRASFTCLA			
NP_835230_P2Y8 (102)	AFYANMYSSILT	MTCISVERFLGVLYPLSSKRWRRRYA	VAAACAG		
TransBD243560_HG52 (102)	AFYANMYSSILT	MTCISVERFLGVLYPLSSKRWRRRYA	VAAACAG		
NP_004092_PAR3 (172)	IFYGNMYCSILLIACISINRYLAI	VHPFTYRGLPKHTYALIVTCGL			
NP_005287_P2Y9 (117)	AFLTNIYGSMFLTCISVD	RELAIVYPFRSRTIRTRNSAIVCAG			
P79928_XP2Y (122)	LFYANLYSSILF	LTCISVHRYRGVCHPITSLLRMNAKHAYVICAL			
Consensus (181)	AFYANMYSSIL	MTCISVDRFLAVVYPLSSKR	R RYAV	CAG	

Section 6

(226)	226	240	250	260	270
AAH18130_PAR1L (198)	TWELLILVLTPEYVVKQIIFIFI	PATNTTCHDVLPEQLE	--VGDMF		
NP_001983_PAR1 (226)	TWALLAAGVVPFLVKEQHIIQVPGIN	TTCHDVLNETLL	--EGYYA		
NP_835230_P2Y8 (147)	TWELLILTALSPIARTDLTYPVHALGH	ITCFDVILKWTMLPSVAMWA			
TransBD243560_HG52 (147)	TWELLILTALSPIARTDLTYPVHALGH	ITCFDVILKWTMLPSVAMWA			
NP_004092_PAR3 (217)	VWATVFLYMLPFFILKQEYLLVQPD	TTCHDVHNTCES	-SSPFQL		
NP_005287_P2Y9 (162)	VWILVLSGGISASLFPST	QVNNAT	--TTCFEGFSKRW	--KTYLS	
P79928_XP2Y (167)	VWLSVTLCLVPNLITFVTVSPKVKN	--TICHDTRPEDF	--ARYV		
Consensus (226)	VWLLVL ALIPL I T V AL	ITTCHDVL	LL A WA		

Section 7

(271)	271	280	290	300	315
AAH18130_PAR1L (241)	NYFLSIATGVFIFPAFLTA	SAYVLMIRMLRSSSAMDENS	--EKKR		
NP_001983_PAR1 (269)	YYFSAFSAVFFFVPLTISTV	CVVSLIRCLSSSAVANRS	--KKS		
NP_835230_P2Y8 (192)	VFLFTIIFILLFI	PPVITVACYTATILKLLRTEEHGR	--EQRR		
TransBD243560_HG52 (192)	VFLFTIIFILLFI	PPVITVACYTATILKLLRTEEHGR	--EQRR		
NP_004092_PAR3 (261)	YYFISI	AFFGFLLPFVLIYCYAAIIRTLN	--AYDHR	--WLWY	
NP_005287_P2Y9 (203)	KITIFIEVVGFI	IPLILNVSCSSVVLRLTRKPATLSQI	--GTNK		
P79928_XP2Y (207)	EMSTA	MCGIFGIPCDIIAGCMGLMTRELMKPIVSGNQQTLPSYK			
Consensus (271)	Y SI ILLFLIP	VITVACY AIIR L KS A R			

Section 8

(316)	316	330	340	350	360
AAH18130_PAR1L (283)	KRAIKLIVSVLAMYLICFTPSNL	LLVVHMFLIKSGQ	--SHV		
NP_001983_PAR1 (311)	--ATFESAAVFCI	FFICFGPTNVLEIAHYSFLSHTST	--TEAA		
NP_835230_P2Y8 (234)	-RAGLAAVVLIAEVTCFA	APNNFVLLAHIVSRLFY	G-----KSY		
TransBD243560_HG52 (234)	-RAGLAAVVLIAEVTCFA	APNNFVLLAHIVSRLFY	G-----KSY		
NP_004092_PAR3 (300)	--VKASLLLILV	ETTCFAPSNIILETHANYYYNN	--TDGL		
NP_005287_P2Y9 (245)	KKVVKM	ITVHMAVFVVCFVPYNSVLFYALVRSQAINTNCFLERFA			
P79928_XP2Y (252)	KRSIKTIIFVMIAFAIC	CFMPFHITRTLYYYARLLGIK	-CYALNVI		
Consensus (316)	RAVKLA	VVLLIFVICFAP	NIVLILHY R		

					Section 9	
	(361)	361	370	380	390	405
AAH18130_PAR1L	(323)	Y A L Y I W A L C L S T L N S C I D P E V Y Y F V S H D F R D H A K N A L L C R S V R				
NP_001983_PAR1	(350)	Y F A Y L L C V C V S S I S S C I D P L I Y Y Y A S S E C Q R Y V Y S I L C C K E S S D				
NP_835230_P2Y8	(272)	Y H V Y K L T L C L S C L N N C L D P E V Y Y F A S R E F Q L R L R E Y L G C R R V P R				
TransBD243560_HG52	(272)	Y H V Y K L T L C L S C L N N C L D P E V Y Y F A S R E F Q L R L R E Y L G C R R V P R				
NP_004092_PAR3	(337)	Y F I Y L I A L C I G S L N S C I D P F L Y E L M S K T R N H S T A Y L T K				
NP_005287_P2Y9	(290)	K I M Y P I T L C L A T L N C C F D P E I Y Y F T L E S F O K S F Y I N A H I R M E S L				
P79928_XP2Y	(296)	N V T Y K V T R P L A S A N S C I D E I L Y F L A N D R Y R R R L I R T V R R R S S V P N				
Consensus	(361)	Y V Y L T L C L S S L N S C I D P F V Y Y F A S E F Q L L C R				
Section 10						
	(406)	406	420	430	440	450
AAH18130_PAR1L	(366)	- - - - T V K Q M Q V S L T S K K H S R K S S Y S S S S T T V K T S Y				
NP_001983_PAR1	(394)	- - - - P S S Y N S S G Q E L M A S K M D T C S S I N L N N S I Y K K L L T				
NP_835230_P2Y8	(316)	- - - - D G L D T R R E S L F S A R T T S V R S E A G A H P E @ M E G A T R P G L Q R Q E				
TransBD243560_HG52	(316)	- - - - D G L D T R R E S L F S A R T T S V R S E A G A H P E @ M E G A T R P G L Q R Q E				
NP_004092_PAR3	(375)	- - - -				
NP_005287_P2Y9	(334)	- - - - F K T E T P L T I K P S L P A I Q E E V S D Q T T N N @ G E L M L E S T F				
P79928_XP2Y	(341)	R R C M H T N H P Q T E P H M T A G P L P V I S A E E I P S N @ S M V R D E N G E G S R E				
Consensus	(406)	T S L S A K S G				
Section 11						
	(451)	451	460	470	480	495
AAH18130_PAR1L	(398)	- - - -				
NP_001983_PAR1	(426)	- - - -				
NP_835230_P2Y8	(357)	S V F - - - -				
TransBD243560_HG52	(357)	S V F - - - -				
NP_004092_PAR3	(375)	- - - -				
NP_005287_P2Y9	(371)	- - - -				
P79928_XP2Y	(386)	H R V E W T D T K E I N Q M M N R R S T I K R N S T D K N D M K E N R H G E N Y L P Y V E				
Consensus	(451)	- - - -				
Section 12						
	(496)	496	510	520	530	540
AAH18130_PAR1L	(398)	- - - -				
NP_001983_PAR1	(426)	- - - -				
NP_835230_P2Y8	(360)	- - - -				
TransBD243560_HG52	(360)	- - - -				
NP_004092_PAR3	(375)	- - - -				
NP_005287_P2Y9	(371)	- - - -				
P79928_XP2Y	(431)	V V E K E D Y E T K R E N R K T T E Q S S K T N A E Q D E L Q T Q I D S R L K R G K W Q L				
Consensus	(496)	- - - -				

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	(541)	<u>541</u>	550	560	570	585	Section 13
AAH18130_PAR1L (398)		- - - - -					
NP_001983_PAR1 (426)		- - - - -					
NP_835230_P2Y8 (360)		- - - - -					
TransBD243560_HG52 (360)		- - - - -					
NP_004092_PAR3 (375)		- - - - -					
NP_005287_P2Y9 (371)		- - - - -					
P79928_XP2Y (476)		S S K K G A A Q E N E K G H M E P S F E G E G T S T W N L L T P K M Y G K K D R L A K N V					
Consensus (541)							
	(586)	<u>586</u>	602				Section 14
AAH18130_PAR1L (398)		- - - - -					
NP_001983_PAR1 (426)		- - - - -					
NP_835230_P2Y8 (360)		- - - - -					
TransBD243560_HG52 (360)		- - - - -					
NP_004092_PAR3 (375)		- - - - -					
NP_005287_P2Y9 (371)		- - - - -					
P79928_XP2Y (521)		E E V G Y G K E K E L Q N F P K A					
Consensus (586)							